

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/730,559B

DATE: 08/09/2001

TIME: 12:36:41

Input Set : A:\766.21 CIP Sequence.txt

Output Set: N:\CRF3\08092001\I730559B.raw

ENTERED

P.5

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4 <110> APPLICANT: ISHIWATA, TETSUYOSHI
5     SAKURADA, MIKIKO
6     KAWABATA, AYAKO
7     NAKAGAWA, SATOSHI
8     NISHI, TATSUNARI
9     KUGA, TETSURO
10    SAWADA, SHIGEMASA
11    TAKEI, MASAMI
12    SHIBATA, KENJI
13    FURUYA, AKIKO
15 <120> TITLE OF INVENTION: IgA NEPHROPATHY-ASSOCIATED GENE
17 <130> FILE REFERENCE: 766.21 CIP
19 <140> CURRENT APPLICATION NUMBER: US 09/730,559B
20 <141> CURRENT FILING DATE: 2000-12-07
22 <160> NUMBER OF SEQ ID NOS: 121
24 <170> SOFTWARE: PatentIn Ver. 2.0
26 <210> SEQ ID NO: 1
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29 <213> ORGANISM: Homo sapiens
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44 ctg ggt tca cct cac tgc ttc agt cac cag aat ggg gag aga gtg gaa 154
45 Leu Gly Ser Pro His Cys Phe Ser His Gln Asn Gly Glu Arg Val Glu
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48 cga tat tct cga aag gtg ttt gta ggc gga ttg cct cca gac att gat 202
49 Arg Tyr Ser Arg Lys Val Phe Val Gly Gly Leu Pro Pro Asp Ile Asp
50 35              40              45              50
52 gaa gat gag atc aca gct agt ttt cgt cgc ttt ggc cct ctg att gtg 250
53 Glu Asp Glu Ile Thr Ala Ser Phe Arg Arg Phe Gly Pro Leu Ile Val
54      55              60              65
56 gat tgg cct cat aaa gct gag agc aaa tcc tat ttt cct cct aaa ggc 298
57 Asp Trp Pro His Lys Ala Glu Ser Lys Ser Tyr Phe Pro Pro Lys Gly
58      70              75              80
60 tat gca ttc ctg ctg ttt caa gat gaa agc tct gtg cag gct ctc att 346
61 Tyr Ala Phe Leu Leu Phe Gln Asp Glu Ser Ser Val Gln Ala Leu Ile
62      85              90              95
64 gat gca tgc att gaa gaa gat gga aaa ctc tac ctt tgt gta tca agt 394
65 Asp Ala Cys Ile Glu Glu Asp Gly Lys Leu Tyr Leu Cys Val Ser Ser

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68 ccc act atc aag gat aag cca gtc cag att cgg cct tgg aat ctc agt 442
69 Pro Thr Ile Lys Asp Lys Pro Val Gln Ile Arg Pro Trp Asn Leu Ser
70 115      120      125      130
72 gac agt gac ttt gtg atg gat ggt tca cag cca ctt gac cca cga aaa 490
73 Asp Ser Asp Phe Val Met Asp Gly Ser Gln Pro Leu Asp Pro Arg Lys
74      135      140      145
76 act ata ttt gtt ggt ggt gtt cct cga cca tta cga gct gtg gag ctt 538
77 Thr Ile Phe Val Gly Gly Val Pro Arg Pro Leu Arg Ala Val Glu Leu
78      150      155      160
80 gcg atg gta atg gat cgg cta tac gga ggt gtg tgc tac gct ggg att 586
81 Ala Met Val Met Asp Arg Leu Tyr Gly Gly Val Cys Tyr Ala Gly Ile
82      165      170      175
84 gat acc gac cct gag cta aaa tac cca aaa gga gct ggg aga gtt gcg 634
85 Asp Thr Asp Pro Glu Leu Lys Tyr Pro Lys Gly Ala Gly Arg Val Ala
86      180      185      190
88 ttc tct aat caa cag agt tac ata gct gct atc agt gcc cgc ttt gtt 682
89 Phe Ser Asn Gln Gln Ser Tyr Ile Ala Ala Ile Ser Ala Arg Phe Val
90 195      200      205      210
92 cag ctg cag cat gga gag ata gat aaa cgg gta agc ctt ata cta cat 730
93 Gln Leu Gln His Gly Glu Ile Asp Lys Arg Val Ser Leu Ile Leu His
94      215      220      225
96 ttt gga aaa ttc tagaaatggt cctctaaatg tgtgattacc aatattagaa 782
97 Phe Gly Lys Phe
98      230
100 cgggagcatt ttatgacaat aaagtgcag ctgacaattt tgcctataga gttaattatg 842
102 gtctataata catgaaataa tgtcctatga atttctttta tctttcagtt ttttgagtag 902
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148 ttgtgttccct ctgcaatgaa atcctttgcc cagtgttcat gtcactctgt agacattatg 2282
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225 &lt;221&gt; NAME/KEY: CDS

226 &lt;222&gt; LOCATION: (107)..(535)

228 &lt;400&gt; SEQUENCE: 2

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232 Met Gly Ser
233 1
235 gac aaa aga gtg agt aga aca gag cgt agt gga aga tac ggt tcc atc 163
236 Asp Lys Arg Val Ser Arg Thr Glu Arg Ser Gly Arg Tyr Gly Ser Ile

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243 gac tca gat tac aaa aga tct agt gat gat cgg agg ggt gat aga tat 259
244 Asp Ser Asp Tyr Lys Arg Ser Ser Asp Asp Arg Arg Gly Asp Arg Tyr
245      40      45      50
247 gat gac tac cga gac tat gac agt cca gag aga gag cgt gaa aga agg 307
248 Asp Asp Tyr Arg Asp Tyr Asp Ser Pro Glu Arg Glu Arg Glu Arg Arg
249      55      60      65
251 aac agt gac cga tcc gaa gat ggc tac cat tca gat ggt gac tat ggt 355
252 Asn Ser Asp Arg Ser Glu Asp Gly Tyr His Ser Asp Gly Asp Tyr Gly
253      70      75      80
255 gag cac gat tat agg cat gac atc agt gac gag agg gag agc aag acc 403
256 Glu His Asp Tyr Arg His Asp Ile Ser Asp Glu Arg Glu Ser Lys Thr
257      85      90      95
259 atc atg ctg cgc ggc ctt ccc atc acc atc aca gag agc gat att cga 451
260 Ile Met Leu Arg Gly Leu Pro Ile Thr Ile Thr Glu Ser Asp Ile Arg
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265      120      125      130
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315 gatttgagtc atccatgaat ccatgaataa aagttacatt ctttgattgg taatattgcc 1925
317 atttataaca agactcacta atgaggggat cactttgact gactgatttg ttaaagtttt 1985

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398 1 5
400 cag ctt att gct gga gga gtt agc aca tcc tgt gtg act gca ctg gga 1362
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404 gag gaa act ggt gcc tgg ttc cct gtg tat ttg tcc cac gcc tcc agt 1410
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## VERIFICATION SUMMARY

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Input Set : A:\766.21 CIP Sequence.txt

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L:1047 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:1150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:1153 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:1499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32  
L:1833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41  
L:1894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43  
L:1912 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44  
L:2848 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:115  
L:2863 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:116  
L:2917 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:120